

# Eliezer Van Allen

## List of Publications by Year in descending order

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Version: 2024-02-01

215  
papers

46,541  
citations

6486

82  
h-index

2584

201  
g-index

247  
all docs

247  
docs citations

247  
times ranked

60257  
citing authors

#	ARTICLE	IF	CITATIONS
1	Implications of Selection Bias Due to Delayed Study Entry in Clinical Genomic Studies. <i>JAMA Oncology</i> , 2022, 8, 287.	3.4	27
2	Inherited TP53 Variants and Risk of Prostate Cancer. <i>European Urology</i> , 2022, 81, 243-250.	0.9	40
3	Integrative clinical and molecular characterization of translocation renal cell carcinoma. <i>Cell Reports</i> , 2022, 38, 110190.	2.9	40
4	Towards a Better Understanding of Antibody-Drug Conjugates in Urothelial Carcinoma. <i>European Urology Oncology</i> , 2022, 5, 719-721.	2.6	1
5	Implementation of a prostate cancer-specific targeted sequencing panel for credentialing of patient-derived cell lines and genomic characterization of patient samples. <i>Prostate</i> , 2022, , .	1.2	1
6	OUP accepted manuscript. <i>Oncologist</i> , 2022, , .	1.9	2
7	Autocrine Canonical Wnt Signaling Primes Noncanonical Signaling through ROR1 in Metastatic Castration-Resistant Prostate Cancer. <i>Cancer Research</i> , 2022, 82, 1518-1533.	0.4	15
8	Linking a Trio of Molecular Features in Clear-Cell Renal Cell Carcinoma. <i>Cancer Immunology Research</i> , 2022, , .	1.6	1
9	Genomic Features of Muscle-invasive Bladder Cancer Arising After Prostate Radiotherapy. <i>European Urology</i> , 2022, 81, 466-473.	0.9	12
10	Concurrent TP53 Mutations Facilitate Resistance Evolution in EGFR-Mutant Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2022, 17, 779-792.	0.5	50
11	Genome-wide analysis of somatic noncoding mutation patterns in cancer. <i>Science</i> , 2022, 376, eabg5601.	6.0	33
12	Insights into Immune Escape During Tumor Evolution and Response to Immunotherapy Using a Rat Model of Breast Cancer. <i>Cancer Immunology Research</i> , 2022, 10, 680-697.	1.6	12
13	CREB5 reprograms FOXA1 nuclear interactions to promote resistance to androgen receptor-targeting therapies. <i>ELife</i> , 2022, 11, .	2.8	10
14	Germline predisposition to pediatric Ewing sarcoma is characterized by inherited pathogenic variants in DNA damage repair genes. <i>American Journal of Human Genetics</i> , 2022, 109, 1026-1037.	2.6	19
15	Molecular profiling identifies targeted therapy opportunities in pediatric solid cancer. <i>Nature Medicine</i> , 2022, 28, 1581-1589.	15.2	16
16	Association of High Tumor Mutation Burden in Non-Small Cell Lung Cancers With Increased Immune Infiltration and Improved Clinical Outcomes of PD-L1 Blockade Across PD-L1 Expression Levels. <i>JAMA Oncology</i> , 2022, 8, 1160.	3.4	117
17	A Process Framework for Ethically Deploying Artificial Intelligence in Oncology. <i>Journal of Clinical Oncology</i> , 2022, 40, 3907-3911.	0.8	6
18	Tissue-resident memory and circulating T cells are early responders to pre-surgical cancer immunotherapy. <i>Cell</i> , 2022, 185, 2918-2935.e29.	13.5	113

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19	Multidimensional Molecular Profiling of Metastatic Triple-Negative Breast Cancer and Immune Checkpoint Inhibitor Benefit. <i>JCO Precision Oncology</i> , 2022, , .	1.5	11
20	Predicting immunotherapy response through genomics. <i>Current Opinion in Genetics and Development</i> , 2021, 66, 1-9.	1.5	12
21	Re: Russell E.N. Becker, Alexa R. Meyer, Aaron Brant, et al. Clinical Restaging and Tumor Sequencing are Inaccurate Indicators of Response to Neoadjuvant Chemotherapy for Muscle-invasive Bladder Cancer. <i>Eur Urol</i> . In press. <a href="https://doi.org/10.1016/j.eururo.2020.07.016">https://doi.org/10.1016/j.eururo.2020.07.016</a> . <i>European Urology</i> , 2021, 79, e56-e57.	0.9	0
22	Identification of a Synthetic Lethal Relationship between Nucleotide Excision Repair Deficiency and Irofulven Sensitivity in Urothelial Cancer. <i>Clinical Cancer Research</i> , 2021, 27, 2011-2022.	3.2	19
23	Dissecting the immunogenomic biology of cancer for biomarker development. <i>Nature Reviews Clinical Oncology</i> , 2021, 18, 133-134.	12.5	7
24	Clinical Efficacy and Molecular Response Correlates of the WEE1 Inhibitor Adavosertib Combined with Cisplatin in Patients with Metastatic Triple-Negative Breast Cancer. <i>Clinical Cancer Research</i> , 2021, 27, 983-991.	3.2	29
25	Integrative molecular characterization of sarcomatoid and rhabdoid renal cell carcinoma. <i>Nature Communications</i> , 2021, 12, 808.	5.8	84
26	Evaluating the molecular diagnostic yield of joint genotyping-based approach for detecting rare germline pathogenic and putative loss-of-function variants. <i>Genetics in Medicine</i> , 2021, 23, 918-926.	1.1	5
27	Transcriptional mediators of treatment resistance in lethal prostate cancer. <i>Nature Medicine</i> , 2021, 27, 426-433.	15.2	90
28	Intrinsic Immunogenicity of Small Cell Lung Carcinoma Revealed by Its Cellular Plasticity. <i>Cancer Discovery</i> , 2021, 11, 1952-1969.	7.7	87
29	Phase II Multicenter Study of Enzalutamide in Metastatic Castration-Resistant Prostate Cancer to Identify Mechanisms Driving Resistance. <i>Clinical Cancer Research</i> , 2021, 27, 3610-3619.	3.2	17
30	Tumor and immune reprogramming during immunotherapy in advanced renal cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 649-661.e5.	7.7	263
31	Evolution of delayed resistance to immunotherapy in a melanoma responder. <i>Nature Medicine</i> , 2021, 27, 985-992.	15.2	67
32	CD38 in Advanced Prostate Cancers. <i>European Urology</i> , 2021, 79, 736-746.	0.9	21
33	Clinical Inflection Point Detection on the Basis of EHR Data to Identify Clinical Trial-Ready Patients With Cancer. <i>JCO Clinical Cancer Informatics</i> , 2021, 5, 622-630.	1.0	3
34	Gene Fusions Create Partner and Collateral Dependencies Essential to Cancer Cell Survival. <i>Cancer Research</i> , 2021, 81, 3971-3984.	0.4	11
35	Discovery and Features of an Alkylating Signature in Colorectal Cancer. <i>Cancer Discovery</i> , 2021, 11, 2446-2455.	7.7	42
36	Correlation Between Surrogate End Points and Overall Survival in a Multi-institutional Clinicogenomic Cohort of Patients With Non-Small Cell Lung or Colorectal Cancer. <i>JAMA Network Open</i> , 2021, 4, e2117547.	2.8	20

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37	Nivolumab in combination with cabozantinib for metastatic triple-negative breast cancer: a phase II and biomarker study. <i>Npj Breast Cancer</i> , 2021, 7, 110.	2.3	20
38	Biologically informed deep neural network for prostate cancer discovery. <i>Nature</i> , 2021, 598, 348-352.	13.7	158
39	Molecular correlates of response to eribulin and pembrolizumab in hormone receptor-positive metastatic breast cancer. <i>Nature Communications</i> , 2021, 12, 5563.	5.8	19
40	RAF1 amplification drives a subset of bladder tumors and confers sensitivity to MAPK-directed therapeutics. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	17
41	Transcriptional profiling of primary prostate tumor in metastatic hormone-sensitive prostate cancer and association with clinical outcomes: correlative analysis of the E3805 CHAARTED trial. <i>Annals of Oncology</i> , 2021, 32, 1157-1166.	0.6	43
42	Integrating molecular profiles into clinical frameworks through the Molecular Oncology Almanac to prospectively guide precision oncology. <i>Nature Cancer</i> , 2021, 2, 1102-1112.	5.7	19
43	Impact of Pathogenic Germline DNA Damage Repair alterations on Response to Intense Neoadjuvant Androgen Deprivation Therapy in High-risk Localized Prostate Cancer. <i>European Urology</i> , 2021, 80, 295-303.	0.9	15
44	Molecular features of exceptional response to neoadjuvant anti-androgen therapy in high-risk localized prostate cancer. <i>Cell Reports</i> , 2021, 36, 109665.	2.9	24
45	Subtype heterogeneity and epigenetic convergence in neuroendocrine prostate cancer. <i>Nature Communications</i> , 2021, 12, 5775.	5.8	59
46	Beyond conventional immune-checkpoint inhibition – novel immunotherapies for renal cell carcinoma. <i>Nature Reviews Clinical Oncology</i> , 2021, 18, 199-214.	12.5	179
47	Integrated Analysis of Germ Cell Tumors. <i>Methods in Molecular Biology</i> , 2021, 2195, 181-187.	0.4	0
48	Tumor Mutations Across Racial Groups in a Real-World Data Registry. <i>JCO Precision Oncology</i> , 2021, 5, 1654-1658.	1.5	16
49	Racial and Ethnic Disparities Among Participants in Precision Oncology Clinical Studies. <i>JAMA Network Open</i> , 2021, 4, e2133205.	2.8	70
50	Artificial intelligence-aided clinical annotation of a large multi-cancer genomic dataset. <i>Nature Communications</i> , 2021, 12, 7304.	5.8	17
51	Genomic attributes of homology-directed DNA repair deficiency in metastatic prostate cancer. <i>JCI Insight</i> , 2021, 6, .	2.3	15
52	A model combining clinical and genomic factors to predict response to PD-1/PD-L1 blockade in advanced urothelial carcinoma. <i>British Journal of Cancer</i> , 2020, 122, 555-563.	2.9	59
53	Prevalence of pathogenic germline cancer risk variants in high-risk urothelial carcinoma. <i>Genetics in Medicine</i> , 2020, 22, 709-718.	1.1	44
54	Natural Language Processing to Ascertain Cancer Outcomes From Medical Oncologist Notes. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 680-690.	1.0	37

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55	Functional Precision Medicine Identifies New Therapeutic Candidates for Medulloblastoma. <i>Cancer Research</i> , 2020, 80, 5393-5407.	0.4	38
56	Accelerating precision medicine in metastatic prostate cancer. <i>Nature Cancer</i> , 2020, 1, 1041-1053.	5.7	45
57	Integrated molecular drivers coordinate biological and clinical states in melanoma. <i>Nature Genetics</i> , 2020, 52, 1373-1383.	9.4	36
58	Detection of Pathogenic Variants With Germline Genetic Testing Using Deep Learning vs Standard Methods in Patients With Prostate Cancer and Melanoma. <i>JAMA - Journal of the American Medical Association</i> , 2020, 324, 1957.	3.8	33
59	A phase 2 trial of buparlisib in patients with platinum-resistant metastatic urothelial carcinoma. <i>Cancer</i> , 2020, 126, 4532-4544.	2.0	14
60	Genomic Predictors of Good Outcome, Recurrence, or Progression in High-Grade T1 Non-Muscle-Invasive Bladder Cancer. <i>Cancer Research</i> , 2020, 80, 4476-4486.	0.4	49
61	Effect of Eribulin With or Without Pembrolizumab on Progression-Free Survival for Patients With Hormone Receptor-Positive, ERBB2-Negative Metastatic Breast Cancer. <i>JAMA Oncology</i> , 2020, 6, 1598.	3.4	84
62	A Systematic Framework to Rapidly Obtain Data on Patients with Cancer and COVID-19: CCC19 Governance, Protocol, and Quality Assurance. <i>Cancer Cell</i> , 2020, 38, 761-766.	7.7	26
63	Germ Cell Tumor Molecular Heterogeneity Revealed Through Analysis of Primary and Metastasis Pairs. <i>JCO Precision Oncology</i> , 2020, 4, 1307-1320.	1.5	9
64	Inactivation of Fbxw7 Impairs dsRNA Sensing and Confers Resistance to PD-1 Blockade. <i>Cancer Discovery</i> , 2020, 10, 1296-1311.	7.7	49
65	Interplay of somatic alterations and immune infiltration modulates response to PD-1 blockade in advanced clear cell renal cell carcinoma. <i>Nature Medicine</i> , 2020, 26, 909-918.	15.2	488
66	Clonal hematopoiesis is associated with adverse outcomes in multiple myeloma patients undergoing transplant. <i>Nature Communications</i> , 2020, 11, 2996.	5.8	98
67	CoMut: visualizing integrated molecular information with comutation plots. <i>Bioinformatics</i> , 2020, 36, 4348-4349.	1.8	39
68	Cancer Moonshot Immuno-Oncology Translational Network (IOTN): accelerating the clinical translation of basic discoveries for improving immunotherapy and immunoprevention of cancer. <i>Nature Reviews Clinical Oncology</i> , 2020, 8, e000796.		7
69	FiTAc-seq: fixed-tissue ChIP-seq for H3K27ac profiling and super-enhancer analysis of FFPE tissues. <i>Nature Protocols</i> , 2020, 15, 2503-2518.	5.5	20
70	Germline Features Associated with Immune Infiltration in Solid Tumors. <i>Cell Reports</i> , 2020, 30, 2900-2908.e4.	2.9	35
71	The role of site-specific therapy for cancers of unknown of primary: A meta-analysis. <i>European Journal of Cancer</i> , 2020, 127, 118-122.	1.3	24
72	Tumor Mutational Burden and PTEN Alterations as Molecular Correlates of Response to PD-1/L1 Blockade in Metastatic Triple-Negative Breast Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 2565-2572.	3.2	138

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73	Single-cell RNA sequencing reveals compromised immune microenvironment in precursor stages of multiple myeloma. <i>Nature Cancer</i> , 2020, 1, 493-506.	5.7	209
74	Mammalian SWI/SNF Complex Genomic Alterations and Immune Checkpoint Blockade in Solid Tumors. <i>Cancer Immunology Research</i> , 2020, 8, 1075-1084.	1.6	47
75	<i>ATM</i> Loss Confers Greater Sensitivity to ATR Inhibition Than PARP Inhibition in Prostate Cancer. <i>Cancer Research</i> , 2020, 80, 2094-2100.	0.4	71
76	Engaging Patients in Precision Oncology: Development and Usability of a Web-Based Patient-Facing Genomic Sequencing Report. <i>JCO Precision Oncology</i> , 2020, 4, 307-318.	1.5	10
77	Identification of cancer driver genes based on nucleotide context. <i>Nature Genetics</i> , 2020, 52, 208-218.	9.4	170
78	Targeting the innate immunoreceptor RIG-I overcomes melanoma-intrinsic resistance to T cell immunotherapy. <i>Journal of Clinical Investigation</i> , 2020, 130, 4266-4281.	3.9	27
79	Genomic Profiling of Smoldering Multiple Myeloma Identifies Patients at a High Risk of Disease Progression. <i>Journal of Clinical Oncology</i> , 2020, 38, 2380-2389.	0.8	110
80	<i>ERCC2</i> Helicase Domain Mutations Confer Nucleotide Excision Repair Deficiency and Drive Cisplatin Sensitivity in Muscle-Invasive Bladder Cancer. <i>Clinical Cancer Research</i> , 2019, 25, 977-988.	3.2	104
81	Assessment of Deep Natural Language Processing in Ascertaining Oncologic Outcomes From Radiology Reports. <i>JAMA Oncology</i> , 2019, 5, 1421.	3.4	99
82	Integrative Molecular Characterization of Resistance to Neoadjuvant Chemoradiation in Rectal Cancer. <i>Clinical Cancer Research</i> , 2019, 25, 5561-5571.	3.2	64
83	Clinical Validation of <i>PBRM1</i> Alterations as a Marker of Immune Checkpoint Inhibitor Response in Renal Cell Carcinoma. <i>JAMA Oncology</i> , 2019, 5, 1631.	3.4	166
84	Metabolomic adaptations and correlates of survival to immune checkpoint blockade. <i>Nature Communications</i> , 2019, 10, 4346.	5.8	139
85	Finding the edge of the seat. <i>Nature Medicine</i> , 2019, 25, 1328-1328.	15.2	0
86	Association of Inherited Pathogenic Variants in Checkpoint Kinase 2 ( <i>CHEK2</i> ) With Susceptibility to Testicular Germ Cell Tumors. <i>JAMA Oncology</i> , 2019, 5, 514.	3.4	43
87	Intrinsic Resistance to Immune Checkpoint Blockade in a Mismatch Repair-Deficient Colorectal Cancer. <i>Cancer Immunology Research</i> , 2019, 7, 1230-1236.	1.6	59
88	Genomic Evolutionary Patterns of Leiomyosarcoma and Liposarcoma. <i>Clinical Cancer Research</i> , 2019, 25, 5135-5142.	3.2	14
89	Genomic correlates of clinical outcome in advanced prostate cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11428-11436.	3.3	839
90	Mechanisms of Resistance to Immune Checkpoint Blockade: Why Does Checkpoint Inhibitor Immunotherapy Not Work for All Patients?. <i>American Society of Clinical Oncology Educational Book / ASCO American Society of Clinical Oncology Meeting</i> , 2019, 39, 147-164.	1.8	459

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91	Genomic correlates of response to immune checkpoint blockade. <i>Nature Medicine</i> , 2019, 25, 389-402.	15.2	346
92	Harmonization of Tumor Mutational Burden Quantification and Association With Response to Immune Checkpoint Blockade in Nonâ€“Small-Cell Lung Cancer. <i>JCO Precision Oncology</i> , 2019, 3, 1-12.	1.5	58
93	Single-cell RNA sequencing reveals compromised immune microenvironment in precursor stages of multiple myeloma. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e27.	0.2	0
94	CREB5 Promotes Resistance to Androgen-Receptor Antagonists and Androgen Deprivation in Prostate Cancer. <i>Cell Reports</i> , 2019, 29, 2355-2370.e6.	2.9	45
95	Integrative molecular and clinical modeling of clinical outcomes to PD1 blockade in patients with metastatic melanoma. <i>Nature Medicine</i> , 2019, 25, 1916-1927.	15.2	541
96	Scaling computational genomics to millions of individuals with GPUs. <i>Genome Biology</i> , 2019, 20, 228.	3.8	108
97	Genomic profiling of smoldering multiple myeloma identifies patients at a high risk of disease progression.. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e5-e6.	0.2	1
98	Compound Genomic Alterations of TP53, PTEN, and RB1 Tumor Suppressors in Localized and Metastatic Prostate Cancer. <i>European Urology</i> , 2019, 76, 89-97.	0.9	158
99	Mutational Analysis of 472 Urothelial Carcinoma Across Grades and Anatomic Sites. <i>Clinical Cancer Research</i> , 2019, 25, 2458-2470.	3.2	102
100	Inherited DNA-Repair Defects in Colorectal Cancer. <i>American Journal of Human Genetics</i> , 2018, 102, 401-414.	2.6	89
101	Integrated genomic characterization of oral carcinomas in post-hematopoietic stem cell transplantation survivors. <i>Oral Oncology</i> , 2018, 81, 1-9.	0.8	8
102	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	13.5	1,670
103	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	13.5	2,111
104	Phase I Trial of a Tablet Formulation of Pilaralisib, a Panâ€“Class I PI3K Inhibitor, in Patients with Advanced Solid Tumors. <i>Oncologist</i> , 2018, 23, 401.	1.9	13
105	Cancer-Germline Antigen Expression Discriminates Clinical Outcome to CTLA-4 Blockade. <i>Cell</i> , 2018, 173, 624-633.e8.	13.5	113
106	Convergent Therapeutic Strategies to Overcome the Heterogeneity of Acquired Resistance in <i>BRAF</i> V600E Colorectal Cancer. <i>Cancer Discovery</i> , 2018, 8, 417-427.	7.7	61
107	Interactive or static reports to guide clinical interpretation of cancer genomics. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2018, 25, 458-464.	2.2	14
108	Genomic correlates of response to immune checkpoint therapies in clear cell renal cell carcinoma. <i>Science</i> , 2018, 359, 801-806.	6.0	898

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109	Whole-exome sequencing of cell-free DNA and circulating tumor cells in multiple myeloma. <i>Nature Communications</i> , 2018, 9, 1691.	5.8	153
110	The long tail of oncogenic drivers in prostate cancer. <i>Nature Genetics</i> , 2018, 50, 645-651.	9.4	601
111	<i>Ex Vivo</i> Profiling of PD-1 Blockade Using Organotypic Tumor Spheroids. <i>Cancer Discovery</i> , 2018, 8, 196-215.	7.7	392
112	Immunogenomic analyses associate immunological alterations with mismatch repair defects in prostate cancer. <i>Journal of Clinical Investigation</i> , 2018, 128, 4441-4453.	3.9	155
113	Enrichment of FGFR3-TACC3 Fusions in Patients With Bladder Cancer Who Are Young, Asian, or Have Never Smoked. <i>JCO Precision Oncology</i> , 2018, 2, 1-11.	1.5	2
114	Genomics of response to immune checkpoint therapies for cancer: implications for precision medicine. <i>Genome Medicine</i> , 2018, 10, 93.	3.6	121
115	A Cancer Cell Program Promotes T Cell Exclusion and Resistance to Checkpoint Blockade. <i>Cell</i> , 2018, 175, 984-997.e24.	13.5	892
116	Everolimus and pazopanib (E/P) benefit genomically selected patients with metastatic urothelial carcinoma. <i>British Journal of Cancer</i> , 2018, 119, 707-712.	2.9	28
117	LSD1 Ablation Stimulates Anti-tumor Immunity and Enables Checkpoint Blockade. <i>Cell</i> , 2018, 174, 549-563.e19.	13.5	473
118	Change in neutrophil-to-lymphocyte ratio (NLR) in response to immune checkpoint blockade for metastatic renal cell carcinoma. , 2018, 6, 5.		200
119	The Clinical Activity of PD-1/PD-L1 Inhibitors in Metastatic Non-“Clear Cell Renal Cell Carcinoma. <i>Cancer Immunology Research</i> , 2018, 6, 758-765.	1.6	89
120	Genomic correlates of response to immune checkpoint blockade in microsatellite-stable solid tumors. <i>Nature Genetics</i> , 2018, 50, 1271-1281.	9.4	438
121	Intron retention is a source of neoepitopes in cancer. <i>Nature Biotechnology</i> , 2018, 36, 1056-1058.	9.4	212
122	A framework to rank genomic alterations as targets for cancer precision medicine: the ESMO Scale for Clinical Actionability of molecular Targets (ESCAT). <i>Annals of Oncology</i> , 2018, 29, 1895-1902.	0.6	424
123	Detection of circulating tumour DNA is associated with inferior outcomes in Ewing sarcoma and osteosarcoma: a report from the Children’s Oncology Group. <i>British Journal of Cancer</i> , 2018, 119, 615-621.	2.9	83
124	Structural Alterations Driving Castration-Resistant Prostate Cancer Revealed by Linked-Read Genome Sequencing. <i>Cell</i> , 2018, 174, 433-447.e19.	13.5	258
125	Early loss of mitochondrial complex I and rewiring of glutathione metabolism in renal oncocyoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6283-E6290.	3.3	70
126	Neoadjuvant-Intensive Androgen Deprivation Therapy Selects for Prostate Tumor Foci with Diverse Subclonal Oncogenic Alterations. <i>Cancer Research</i> , 2018, 78, 4716-4730.	0.4	56



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127	The Role of Clonal Hematopoiesis of Indeterminate Potential (CHIP) in Multiple Myeloma: Immunomodulator Maintenance Post Autologous Stem Cell Transplant (ASCT) Predicts Better Outcome. <i>Blood</i> , 2018, 132, 749-749.	0.6	6
128	Single-Cell RNA Sequencing Reveals Compromised Immune Microenvironment in Precursor Stages of Multiple Myeloma. <i>Blood</i> , 2018, 132, 2603-2603.	0.6	1
129	Assigning clinical meaning to somatic and germ-line whole-exome sequencing data in a prospective cancer precision medicine study. <i>Genetics in Medicine</i> , 2017, 19, 787-795.	1.1	46
130	Loss of PTEN Is Associated with Resistance to Anti-PD-1 Checkpoint Blockade Therapy in Metastatic Uterine Leiomyosarcoma. <i>Immunity</i> , 2017, 46, 197-204.	6.6	400
131	Phase 2 trial of sunitinib and gemcitabine in patients with sarcomatoid and/or poor-risk metastatic renal cell carcinoma. Michaelson MD, McKay RR, Werner L, Atkins MB, Van Allen EM, Olivier KM, Song J, Signoretti S, McDermott DF, Choueiri TK. <i>Cancer</i> . 2015 Oct 1;121(19):3435-43. [Epub 2015 Jun 8]. doi: 10.1002/ncr.29503. <i>Urologic Oncology: Seminars and Original Investigations</i> . 2017. 35. 117-118.	0.8	5
132	Exome Sequencing of African-American Prostate Cancer Reveals Loss-of-Function <i>ERF</i> Mutations. <i>Cancer Discovery</i> , 2017, 7, 973-983.	7.7	94
133	Toward Molecularly Driven Precision Medicine in Lung Adenocarcinoma. <i>Cancer Discovery</i> , 2017, 7, 555-557.	7.7	11
134	The Mutational Landscape of Circulating Tumor Cells in Multiple Myeloma. <i>Cell Reports</i> , 2017, 19, 218-224.	2.9	92
135	The fuzzy world of precision medicine: deliberations of a precision medicine tumor board. <i>Personalized Medicine</i> , 2017, 14, 37-50.	0.8	15
136	Somatic Mutations and Neopeptide Homology in Melanomas Treated with CTLA-4 Blockade. <i>Cancer Immunology Research</i> , 2017, 5, 84-91.	1.6	126
137	Decomposing Oncogenic Transcriptional Signatures to Generate Maps of Divergent Cellular States. <i>Cell Systems</i> , 2017, 5, 105-118.e9.	2.9	40
138	The Potential and Challenges of Expanded Germline Testing in Clinical Oncology. <i>JAMA - Journal of the American Medical Association</i> , 2017, 318, 801.	3.8	6
139	In vivo CRISPR screening identifies Ptpn2 as a cancer immunotherapy target. <i>Nature</i> , 2017, 547, 413-418.	13.7	792
140	Genomic profiling of ER <sup>+</sup> breast cancers after short-term estrogen suppression reveals alterations associated with endocrine resistance. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	91
141	Tumor Evolution: A Problem of Histocompatibility. <i>Cell</i> , 2017, 171, 1252-1253.	13.5	5
142	Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. <i>Nature Communications</i> , 2017, 8, 1324.	5.8	584
143	Genomic Heterogeneity and Exceptional Response to Dual Pathway Inhibition in Anaplastic Thyroid Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 2367-2373.	3.2	24
144	Genomic Evolution after Chemoradiotherapy in Anal Squamous Cell Carcinoma. <i>Clinical Cancer Research</i> , 2017, 23, 3214-3222.	3.2	44

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145	Mutational patterns in chemotherapy resistant muscle-invasive bladder cancer. <i>Nature Communications</i> , 2017, 8, 2193.	5.8	99
146	Genomic Resistance Patterns to Second-Generation Androgen Blockade in Paired Tumor Biopsies of Metastatic Castration-Resistant Prostate Cancer. <i>JCO Precision Oncology</i> , 2017, 1, 1-11.	1.5	13
147	Systematic genomic and translational efficiency studies of uveal melanoma. <i>PLoS ONE</i> , 2017, 12, e0178189.	1.1	34
148	Precision medicine for advanced prostate cancer. <i>Current Opinion in Urology</i> , 2016, 26, 231-239.	0.9	23
149	Inherited DNA-Repair Gene Mutations in Men with Metastatic Prostate Cancer. <i>New England Journal of Medicine</i> , 2016, 375, 443-453.	13.9	1,205
150	A phase 1 study of buparlisib and bevacizumab in patients with metastatic renal cell carcinoma progressing on vascular endothelial growth factor-targeted therapies. <i>Cancer</i> , 2016, 122, 2389-2398.	2.0	16
151	Genomic evolution and chemoresistance in germ-cell tumours. <i>Nature</i> , 2016, 540, 114-118.	13.7	139
152	Dissecting the multicellular ecosystem of metastatic melanoma by single-cell RNA-seq. <i>Science</i> , 2016, 352, 189-196.	6.0	3,421
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